

5' TTT AAG TAG GCT ATA AAA ATC AAG TTG CTG TCT TCA GAG GGT CTG TGG TCC TCT  
           9      18      27      36      45      54  
       63      72      81      90      99      108  
       GAT CAA CAT AGG CTG GTG GGA GTA CAG GAC TCG CCT CCT CAG GGT TCC CTG TGC  
       117      126      135      144      153      162  
       TGC CAC TTT TCA GCC ATG GCC ACA AGT GAA CAG ACT ATC TGC CAA GCC CGG GCT  
       M      A      T      S      E      Q      S      I      C      Q      A      R      A  
       171      180      189      198      207      216  
       TCC GTG ATG GTC TAC GAT GAC ACC AGT AAG AAA TGG GTA CCA ATC AAA CCT GGC  
       S      V      M      V      D      T      S      K      K      W      V      P      I      K      P      G  
       225      234      243      252      261      270  
       CAG CAG GGA TTC AGC CGG ATC AAC ATC TAC CAC AAC ACT GCC AGC AAC ACC TTC  
       Q      Q      G      F      S      R      I      N      I      Y      H      N      T      A      S      N      T      F  
       279      288      297      306      315      324  
       AGA GTC GTT GGA GTC AAG TTG CAG GAT CAG CAG GTP GTG ATC AAT TAT TCA ATC  
       R      V      V      G      V      K      L      Q      D      Q      Q      V      V      I      N      Y      S      I  
       333      342      351      360      369      378  
       GTG AAA GGG CTG AAG TAC AAT CAG GCC ACG CCA ACC TTC CAC CAG TGG CGA GAT  
       V      K      G      L      K      Y      N      Q      A      T      P      T      F      H      Q      W      R      D

FIGURE 1A

	387	396	405	414	423	432											
GCC	CGC	CAG	GTC	TAC	GGC	TTA	AAC	TTT	GCA	AGT	AAA	GAA	GAG	GCA	ACC	ACG	TTC
A	R	Q	V	Y	G	L	N	F	A	S	K	E	E	A	T	T	F
	441	450	459	468	477	486											
TCC	AAT	GCA	ATG	CTG	TTT	GCC	CTG	AAC	ATC	ATG	AAT	TCC	CAA	GAA	GGA	GCG	CCC
S	N	A	M	L	F	A	L	N	I	M	N	S	Q	E	G	G	P
	495	504	513	522	531	540											
TCC	AGC	CAG	CGT	CAG	GTG	CAG	GGC	CCC	TCT	CCT	GAT	GAG	ATG	GAC	ATC	CAG	
S	S	Q	R	Q	V	Q	N	G	P	S	P	D	E	M	D	I	Q
	549	558	567	576	585	594											
AGA	AGA	CAA	GTG	GAG	CAC	CAG	CAG	CAG	CAG	CGT	CAG	GAA	TCT	CTA	GAA	AGA	
R	R	Q	V	M	E	Q	H	Q	Q	R	Q	E	S	L	E	R	
	603	612	621	630	639	648											
AGA	ACC	TGC	GCC	ACA	GGG	CCC	ATC	CTC	CCA	CCA	CAT	CCT	TCA	TCT	GCA	GCC	
R	T	S	A	T	G	P	I	L	P	P	G	H	P	S	S	A	A
	657	666	675	684	693	702											
AGC	GCC	CCC	GTC	TCA	TGT	AGT	GGG	CCT	CCA	CCG	CCC	CCA	CCT	CTA	GTC	CCA	
S	A	P	V	S	C	S	G	P	P	P	P	P	P	L	V	P	
	711	720	729	738	747	756											
CCT	CCA	CCC	ACT	GGG	GCT	ACC	CCA	CCT	CCC	CCA	CTG	CCA	GCC	GGA	GGA		
P	P	P	T	G	A	T	P	P	P	P	L	P	A	G	G		

FIGURE 1B

	765	774	783	792	801	810
GCC	CAG	TGG	TCC	AGC	CAC	GAC
A	Q	S	S	H	D	E
				S	S	S
				M	S	G
				S	G	L
					A	A
					A	I
	819	828	837	846	855	864
GCT	GGG	GCC	AAG	CTG	AGA	GTC
A	G	A	K	L	R	V
				R	Q	R
					P	P
					E	E
					D	A
					S	S
					G	G
					S	S
	873	882	891	900	909	918
AGT	CCC	AGT	GGG	ACC	TCA	AAG
S	P	S	G	T	S	K
					D	A
					N	R
					A	S
					S	G
					G	G
					G	G
	927	936	945	954	963	972
GGA	GGA	GCG	CTC	ATG	GAG	AAC
G	G	G	L	M	E	M
				N	N	K
					K	L
					A	L
					K	A
					R	R
					R	R
					K	A
	981	990	999	1008	1017	1026
GCC	TCC	CAG	TCA	GAC	AAG	GAA
A	S	Q	S	D	K	P
					A	E
					E	K
					D	E
					S	Q
					M	M
					E	E
	1035	1044	1053	1062	1071	1080
GAT	CCT	AGT	ACC	TCC	CCC	TCT
D	P	S	T	S	P	S
	1089	1098	1107	1116	1125	1134
TCC	TCA	GAG	GCT	GGC	CGG	AAG
S	S	E	A	G	R	K
					P	W
					S	E
					V	E
					K	P

FIGURE 1C

1143	GTG TCC TCG ATT CTG TCC AGA ACC CCG TCT GTG GCA AAG AGC CCC GAA GCT AAG	1161	1170	1179	1188	
V S S I L S R T P S V A K S P E A K						
1197	AGC CCC CTT CAG TCG CAG CCT CAC TCT AGG ATG AAG CCT GCT GGG AGC GTG AAT	1206	1215	1224	1233	1242
S P L Q S Q P H S R M K P A G S V N						
1251	GAC ATG GCC CTG GAT GCC TTC GAC TTG GAC CGG ATG AAG CAG GAG ATC CTA GAG	1260	1269	1278	1287	1296
D M A L D A F D L D R M K Q E I L E						
1305	GAG GTG AGA GAG CTC CAC AAG GTG AAG GAG ATC ATC GAC GCC ATC AGG	1314	1323	1332	1341	1350
E V V R E L H K V K E E I I D A I R						
1359	CAG GAG CTG AGT GGG ATC AGC ACC ACG TAA GGG GCC GGC CTC GCT GCG CTG ATT	1368	1377	1386	1395	1404
Q E L S G I S T T						
1413	CGT CGA GCC CAT CCG GCG ACA GAG GAC AGC CAG AAG CCC AGC CAG CCC CAG ACT	1422	1431	1440	1449	1458
1467	CCA GTG CAC CAG AGC ACG CAC AGG AGC CTG GGC GCG CTG CTG TGA AAC GTC CTC	1476	1485	1494	1503	1512

FIGURE 1D

1521      1530      1539      1548      1557      1566  
 ACC TGT GAT CAC ACA TGA CAG TGA GGA AAC CAA GRG CAA CTC CTG GGT TTT TTT  
  
 1575      1584      1593      1602      1611      1620  
 TAG ATT CTG CCT GAC ACG GAA CAC CAG GTC TGC TCG TCT TTT TTG TGT TTT ATA  
  
 1629      1638      1647      1656      1665      1674  
 TTT GCT TAT TTA AGG TAC ATT TCT TTT GGT TTG AGA CGC CCC TAA GTC ACC  
  
 1683      1692      1701      1710      1719      1728  
 TGC TTC ATT AGA CGG TTT CCA GGT TTT CTC CCA GGT GAC GCT GTT AGC GCC TCA  
  
 1737      1746      1755      1764      1773      1782  
 GCT GGC GGT GAC AGC CGG CCC AGC GTG GCG CCA CCA CAC ACC GCA GAG CTG TCC  
  
 1791      1800      1809      1818      1827      1836  
 AGG CAC AGC TCC GTC CCC AGC GCT CAT GGT GAA ACT GTC TGT CAT GCA CCA  
  
 1845      1854      1863      1872      1881  
 CGG TGT CTG TGT CCA CAC AGT AAT AAA CGG TTT ACT GTC CGC AAA AAA AA 3'

FIGURE 1E

1 MATSEQSICQARASVMVYDDTSKKWVPIK P 3089412  
 1 M - SEQSICQARASVMVYDDTSKKWVPIK P GT 1644453  
 1 M - SE[TVICSSRATVMLYDDGNGK[RWL[PAG T GT 624964

31 GQQGF S R I N I Y H N T A S N T F R V V G V K L Q - D Q 3089412  
 29 GQQGF S R I N I Y H N T A S S T F R V V G V K L Q - D Q 3089412  
 29 G P Q [A F S R V Q I Y H N P T A N S F R V V G R K M Q P D Q GT 624964

60 Q V V I N Y S I V K G L K Y N Q A T P T F H Q W R D A R Q V 3089412  
 58 Q V V I N Y S I V K G L K Y N Q A T P T F H Q W R D A R Q V 3089412  
 59 Q V V I N C A I V R G [V K Y N Q A T P N F H Q W R D A R Q V 3089412  
 90 Y G L N F A S K E E A T T F S N A M I L F A L N I M N S Q E G 3089412  
 88 Y G L N F A S K E E A T T F S N A M I L F A L N I M N S Q E G 3089412  
 89 W G L N F G S K E D D A Q F A A G M A S A L E A L E G G G P GT 624964

120 G P S S Q - - R Q V Q N G P S P D E M D I Q R R Q V M E Q 3089412  
 118 G P S T Q - - R Q V Q N G P S P E E M D I Q R R Q V M E Q 3089412  
 119 P P P P A L P T W S V P N G P S P E E V E Q Q [K R Q - - - GI 624964

147 H Q Q Q R Q E S L E R R T S A T G P I L P P G H P S S A A S 3089412  
 145 - Q H R Q E S L E R R T I S A T G P I L P P G H P S S A A S 3089412  
 145 - Q P G P S E H I E R R V S N A G G - - P P A P P A G G P P GT 624964

FIGURE 2A

FIGURE 2B

Docket No.: PF-0471-3 DIV

Inventors: Lal et al.

Title: HUMAN ENA/VASP-LIKE PROTEIN SPlice VARIANT

Serial No.: To Be Assigned

349	A K S P E A K S P L Q S O P H S R M K P A G S V N D M A L D	3089412
341	- - - - -	
321	- [K S] S S V T T S E T [Q P] C T P S S - - - - -	[V K P A G S V N D V G L D] GI 1644453 [D] GI 624964
379	A F D L D R M K Q E I L E E V V R E L H K V K E E I I D A I	3089412
354	A [L D L D R M K Q E I L E E V V R E L H K V K E E I I D A I	GI 1644453
341	Y S D L [Q R] V K Q E L L E E V K K E L [Q K V K E E I I E A F	GI 624964
409	R Q E L S G I S T T	3089412
384	R Q E L S G I S T T	GI 1644453
371	V Q E L R K R G S P	GI 624964

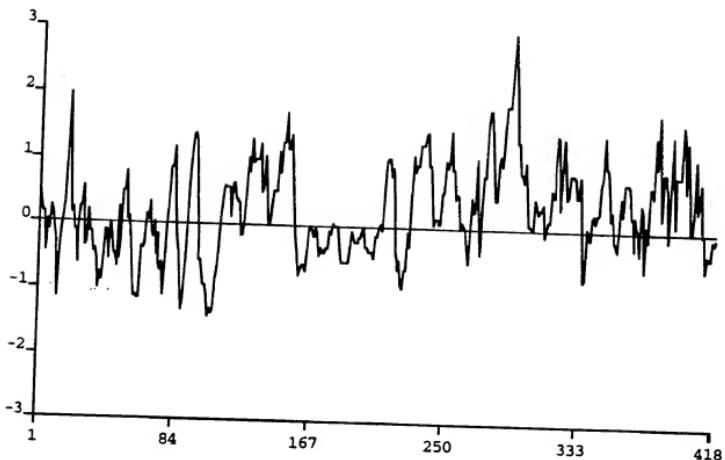
FIGURE 2C

Docket No.: PF-0471-3 DIV

Inventors: Lal et al.

Title: HUMAN ENA/VASP-LIKE PROTEIN SPlice VARIANT

Serial No.: To Be Assigned



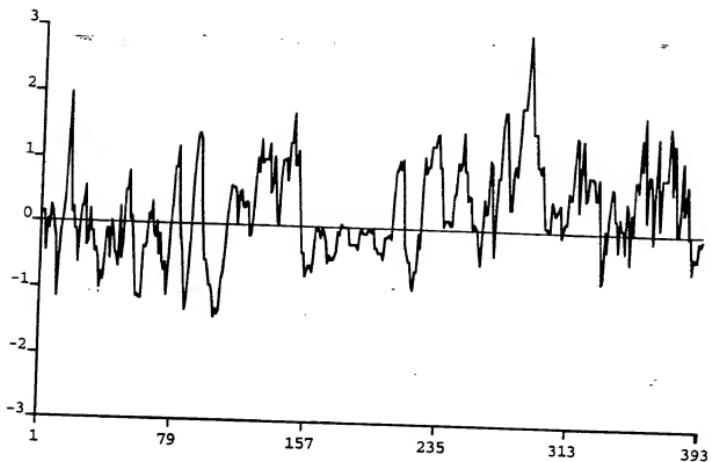
**FIGURE 3A**

Docket No.: PF-0471-3 DIV

Inventors: Lal et al.

Title: HUMAN ENA/VASP-LIKE PROTEIN SPLICE VARIANT

Serial No.: To Be Assigned



**FIGURE 3B**